

Input Set: I913878.RAW

This Raw Listing contains the Gen ral Information
Section and up to first 5 pag s.

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MAY 08 2003

TECH CENTER 1600/2900

1 <110> APPLICANT: Universit degli Studi di Roma La Sapienza
2 Macino Giuseppe
3 Cogoni Carlo
4 <120> TITLE OF INVENTION: Isolation and characterization of a N. crassa silencing
5 gene and uses thereof
6 <130> FILE REFERENCE: macino2
7 <140> CURRENT APPLICATION NUMBER: US/09/913,878
8 <141> CURRENT FILING DATE: 2001-08-20
9 <150> EARLIER APPLICATION NUMBER: RM99A000117
10 <151> EARLIER FILING DATE: 1999-02-22
11 <160> NUMBER OF SEQ ID NOS: 2
12 <170> SOFTWARE: PatentIn Ver. 2.1
13 <210> SEQ ID NO 1
14 <211> LENGTH: 8045
15 <212> TYPE: DNA
16 <213> ORGANISM: Neurospora crassa
17 <220> FEATURE:
18 <221> NAME/KEY: CDS
19 <222> LOCATION: (2447)..(6655)
20 <400> SEQUENCE: 1
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23 ccgaataggt tcgtacgctg tcccctttag ggggctggtt taacagggag acaggggtaca 180
24 gtctctcggg aacagagacg accaagcttt gttgtgtgac atcatcttga gaccattcgt 240
25 ctgaggggtcc atacaaccat acatgctgtg tagagagtgg tgggaatatt agaggttact 300
26 ttgagagttt ctgaagagat tgagactgta ggtacgttca tttatcgggtg cgacgagaat 360
27 gggcacgcat gagtcgacat ttgcaatttg ttggttgga cgcacatcga tagtgtacac 420
28 atgtgtcggc ctgagactgt ccaatggacc aatggtaagg cgtgagcggc gagggtgggc 480
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34 cgagacccca atcagtatga ccgacagcga caccatcacc ggcgccagcg tatgagatcc 840
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39 cgctgacagg gcaccgtgct gcctggacct ttgcgggccc ttccttcttg accggcgcca 1140
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RAW SEQUENCE LISTING PATENT APPLICATION US/09/913,878

DATE: 09/10/2
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61 aaccgggttg tatactctac tccaggcccc atctcccacg gcacaa atg aac cct 2455
62                                     Met Asn Pro
63                                     1
64 att act cct agg aag agg aat agc ccc gtc gag gaa atc ata aac cgg 2503
65 Ile Thr Pro Arg Lys Arg Asn Ser Pro Val Glu Glu Ile Ile Asn Arg
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67 ctc aat aac gac tac aac ctg ggc ctc cag tgt gtc gca gac aca act 2551
68 Leu Asn Asn Asp Tyr Asn Leu Gly Leu Gln Cys Val Ala Asp Thr Thr
69      20              25              30              35
70 ctc acc ccc cac cgc cgg aag gag ctg gcc gag agt gac gag gat ttc 2599
71 Leu Thr Pro His Arg Arg Lys Glu Leu Ala Glu Ser Asp Glu Asp Phe
72      40              45              50
73 ggt cgc cat gac aag atc tac aga gcc ctg aac ttt ctc tac tgg cgg 2647
74 Gly Arg His Asp Lys Ile Tyr Arg Ala Leu Asn Phe Leu Tyr Trp Arg
75      55              60              65
76 aag gat gac tcc ctg aac cag gca gaa gcc aac ttc ttc atc gag gcc 2695
77 Lys Asp Asp Ser Leu Asn Gln Ala Glu Ala Asn Phe Phe Ile Glu Ala
78      70              75              80
79 aaa gct gcg agc tcg aac tgg gtg ccc aaa gcc cac gcc gac cct gac 2743
80 Lys Ala Ala Ser Ser Asn Trp Val Pro Lys Ala His Ala Asp Pro Asp
81      85              90              95
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83 Thr Leu Pro Trp Ser Lys Glu Pro Pro Arg Ala Ala Thr Ala Gly Gln
84      100              105              110              115
85 caa tgg gca ttg cag act gtg ttg ctc gag gtg ctt aat agg ttt atg 2839
86 Gln Trp Ala Leu Gln Thr Val Leu Leu Glu Val Leu Asn Arg Phe Met
87      120              125              130
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89 Pro Pro Pro Asn Asn Thr Pro Gly Arg Thr Phe Gly Arg Thr Leu Ser
90      135              140              145
91 ggc cca agt ggc ctg agc cgc cca acc tct acc aac acc aaa cgc aag 2935
92 Gly Pro Ser Gly Leu Ser Arg Pro Thr Ser Thr Asn Thr Lys Arg Lys
93      150              155              160
94 gat gag ccc gcc aat gtc act ttc gct gat ccg ccc aaa cgc tcg ttg 2983

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98	Thr Arg Ser Ala Thr Gly Pro Pro Ile His Gly Ala Ala Ile Pro Leu	
99	180 185 190 195	
100	aag ttc ccc gat cca gtg aat acc ggt tcc aaa cga cca tct ctc gag	3079
101	Lys Phe Pro Asp Pro Val Asn Thr Gly Ser Lys Arg Pro Ser Leu Glu	
102	200 205 210	
103	agt gag aat ctc aat cag tgc acc aag cgg gcc aag ggc aag ctg tct	3127
104	Ser Glu Asn Leu Asn Gln Cys Thr Lys Arg Ala Lys Gly Lys Leu Ser	
105	215 220 225	
106	gat aat gtt gcc gct gcc gcc gcc ccg ccc gtg cct att gcg agc gct	3175
107	Asp Asn Val Ala Ala Ala Ala Ala Pro Pro Val Pro Ile Ala Ser Ala	
108	230 235 240	
109	ttg gac aag gta ccg act cga agg cat gcc aat acg aga gat ccc acg	3223
110	Leu Asp Lys Val Pro Thr Arg Arg His Ala Asn Thr Arg Asp Pro Thr	
111	245 250 255	
112	gcg aca ggt cat aga cga gcg gac cag gtg gat tcc ttt gat aca tct	3271
113	Ala Thr Gly His Arg Arg Ala Asp Gln Val Asp Ser Phe Asp Thr Ser	
114	260 265 270 275	
115	caa ggc act tcc tat ggt tcg agt gtc ttc agc gct tgc cgt cac aat	3319
116	Gln Gly Thr Ser Tyr Gly Ser Ser Val Phe Ser Ala Cys Arg His Asn	
117	280 285 290	
118	cag agc act acc cag agt agt ttt gag gct cct cct tca cag ccc aga	3367
119	Gln Ser Thr Thr Gln Ser Ser Phe Glu Ala Pro Pro Ser Gln Pro Arg	
120	295 300 305	
121	gag aag cgg cct gtg gat gcc acg gtc ttt gag gct gga cac ttg att	3415
122	Glu Lys Arg Pro Val Asp Ala Thr Val Phe Glu Ala Gly His Leu Ile	
123	310 315 320	
124	gag tct cct agc aaa gga aga aca acc aag tcc cac ata gat aac cag	3463
125	Glu Ser Pro Ser Lys Gly Arg Thr Thr Lys Ser His Ile Asp Asn Gln	
126	325 330 335	
127	ccc ctt tca tcg tct tcc cag ggt gaa act tcg ttc agc act tac tat	3511
128	Pro Leu Ser Ser Ser Ser Gln Gly Glu Thr Ser Phe Ser Thr Tyr Tyr	
129	340 345 350 355	
130	gag tcg ttt cca agt tcc ggc ggc gag ggc gca att ccc gag ccg agt	3559
131	Glu Ser Phe Pro Ser Ser Gly Gly Glu Gly Ala Ile Pro Glu Pro Ser	
132	360 365 370	
133	cgc tca aat gga ctg gct cgg agc gaa gaa agc gct cga tct cag gtt	3607
134	Arg Ser Asn Gly Leu Ala Arg Ser Glu Glu Ser Ala Arg Ser Gln Val	
135	375 380 385	
136	caa gtt cat gcc ccg gtg gtt gca gct cgg ctg aga aat att tgg ccg	3655
137	Gln Val His Ala Pro Val Val Ala Ala Arg Leu Arg Asn Ile Trp Pro	
138	390 395 400	
139	aaa ttt ccc aaa tgg cta cac gaa gct cct ctc gct gtt gca tgg gaa	3703
140	Lys Phe Pro Lys Trp Leu His Glu Ala Pro Leu Ala Val Ala Trp Glu	
141	405 410 415	
142	gtt acc aga ctc ttt atg cac tgc aaa gta gac ttg gaa gac gag agc	3751
143	Val Thr Arg Leu Phe Met His Cys Lys Val Asp Leu Glu Asp Glu Ser	
144	420 425 430 435	

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147	440 445 450	
148	gat atc tgg aag act ctc tac cgg ctt gat gct ttc cgt ggt aaa ccc	3847
149	Asp Ile Trp Lys Thr Leu Tyr Arg Leu Asp Ala Phe Arg Gly Lys Pro	
150	455 460 465	
151	ttt cca gaa aag ccg ccc aac gac gtg ttc gtg acc gca atg acg ggc	3895
152	Phe Pro Glu Lys Pro Pro Asn Asp Val Phe Val Thr Ala Met Thr Gly	
153	470 475 480	
154	aac ttt gag agc aaa ggt agt gcc gtt gtt ctc tct gct gtt cta gac	3943
155	Asn Phe Glu Ser Lys Gly Ser Ala Val Val Leu Ser Ala Val Leu Asp	
156	485 490 495	
157	tac aat ccg gac aac tcg cct act gcg ccc ctt tac ctt gtg aag ctg	3991
158	Tyr Asn Pro Asp Asn Ser Pro Thr Ala Pro Leu Tyr Leu Val Lys Leu	
159	500 505 510 515	
160	aag ccg ctc atg ttc gag cag ggc tgt cga ctc acc cgt cgg ttc ggt	4039
161	Lys Pro Leu Met Phe Glu Gln Gly Cys Arg Leu Thr Arg Arg Phe Gly	
162	520 525 530	
163	cct gat agg ttt ttc gag atc ctt ata ccg tcg cct acg agc acc agc	4087
164	Pro Asp Arg Phe Phe Glu Ile Leu Ile Pro Ser Pro Thr Ser Thr Ser	
165	535 540 545	
166	cca agt gta ccg ccg gtg gtc agc aaa caa cca ggt gcg gtc gaa gaa	4135
167	Pro Ser Val Pro Pro Val Val Ser Lys Gln Pro Gly Ala Val Glu Glu	
168	550 555 560	
169	gtc atc cag tgg ctc acg atg ggg caa cat tct ctt gta ggc cgc caa	4183
170	Val Ile Gln Trp Leu Thr Met Gly Gln His Ser Leu Val Gly Arg Gln	
171	565 570 575	
172	tgg cgc gct ttc ttc gcc aaa gat gcc gga tac agg aaa cct ctc agg	4231
173	Trp Arg Ala Phe Phe Ala Lys Asp Ala Gly Tyr Arg Lys Pro Leu Arg	
174	580 585 590 595	
175	gag ttc cag ctc cgc gcc gag gac ccg aaa ccc atc atc aag gag aga	4279
176	Glu Phe Gln Leu Arg Ala Glu Asp Pro Lys Pro Ile Ile Lys Glu Arg	
177	600 605 610	
178	gtc cac ttc ttt gcc gag acc ggc att acg ttc cga cct gat gtg ttc	4327
179	Val His Phe Phe Ala Glu Thr Gly Ile Thr Phe Arg Pro Asp Val Phe	
180	615 620 625	
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185	Glu Phe Lys Val Ser Gln Met Leu Asp Trp Leu Leu Gln Leu Asp Asn	
186	645 650 655	
187	aac act tgg cag ccg cac ctc aag ttg ttc tcc cgt atc cag ctc ggt	4471
188	Asn Thr Trp Gln Pro His Leu Lys Leu Phe Ser Arg Ile Gln Leu Gly	
189	660 665 670 675	
190	ctg agt aag aca tat gcc att atg aca ttg gag cct cac cag atc aga	4519
191	Leu Ser Lys Thr Tyr Ala Ile Met Thr Leu Glu Pro His Gln Ile Arg	
192	680 685 690	
193	cac cac aag acc gat ctt ctt tca cct tca ggc act ggc gaa gtg atg	4567
194	His His Lys Thr Asp Leu Leu Ser Pro Ser Gly Thr Gly Glu Val Met	

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198	710	715	720	
199	gat gtt ctc ggt ttg ggt gat gtg ccc tct gct gtg caa ggg cgg ttt			4663
200	Asp Val Leu Gly Leu Gly Asp Val Pro Ser Ala Val Gln Gly Arg Phe			
201	725	730	735	
202	ggt tgc gcc aag gga atg tgg gtt atc gac gtt gac gac aca ggc gat			4711
203	Gly Ser Ala Lys Gly Met Trp Val Ile Asp Val Asp Asp Thr Gly Asp			
204	740	745	750	755
205	gag gat tgg atc gag aca tac ccg tcc cag cgc aag tgg gaa tgc gac			4759
206	Glu Asp Trp Ile Glu Thr Tyr Pro Ser Gln Arg Lys Trp Glu Cys Asp			
207	760	765	770	
208	ttc gtt gat aaa cat caa cgt acc ctc gaa gtc cgg agc gtg gct tct			4807
209	Phe Val Asp Lys His Gln Arg Thr Leu Glu Val Arg Ser Val Ala Ser			
210	775	780	785	
211	gaa ctg aag tca gct ggt ctc aac cta cag ctg tta cct gtc ctg gaa			4855
212	Glu Leu Lys Ser Ala Gly Leu Asn Leu Gln Leu Leu Pro Val Leu Glu			
213	790	795	800	
214	gat aga gcc agg gac aag gtg aag atg cgc cag gca atc ggt gac cgt			4903
215	Asp Arg Ala Arg Asp Lys Val Lys Met Arg Gln Ala Ile Gly Asp Arg			
216	805	810	815	
217	ctt atc aac gat ttg caa cga cag ttc agc gag caa aag cat gct ttg			4951
218	Leu Ile Asn Asp Leu Gln Arg Gln Phe Ser Glu Gln Lys His Ala Leu			
219	820	825	830	835
220	aat cgc cca gtg gaa ttt cgc caa tgg gtt tac gag agt tat tcc agt			4999
221	Asn Arg Pro Val Glu Phe Arg Gln Trp Val Tyr Glu Ser Tyr Ser Ser			
222	840	845	850	
223	cgc gca act cga gtc agc cac ggc cgt gtg cct ttt ctt gct ggg cta			5047
224	Arg Ala Thr Arg Val Ser His Gly Arg Val Pro Phe Leu Ala Gly Leu			
225	855	860	865	
226	cct gac agt caa gag gag aca ctg aac ttc ttg atg aac agt ggg ttc			5095
227	Pro Asp Ser Gln Glu Glu Thr Leu Asn Phe Leu Met Asn Ser Gly Phe			
228	870	875	880	
229	gat ccc aag aag caa aag tac ttg caa gac atc gcc tgg gat ctt caa			5143
230	Asp Pro Lys Lys Gln Lys Tyr Leu Gln Asp Ile Ala Trp Asp Leu Gln			
231	885	890	895	
232	aag cgg aaa tgt gac acg ttg aag tcc aag ctg aac atc cgt gtc ggt			5191
233	Lys Arg Lys Cys Asp Thr Leu Lys Ser Lys Leu Asn Ile Arg Val Gly			
234	900	905	910	915
235	cga tca gca tac att tac atg att gcc gat ttc tgg ggt gtg ctt gag			5239
236	Arg Ser Ala Tyr Ile Tyr Met Ile Ala Asp Phe Trp Gly Val Leu Glu			
237	920	925	930	
238	gaa aat gag gtt cat gtc gga ttc tcc tca aag ttc aga gac gag gag			5287
239	Glu Asn Glu Val His Val Gly Phe Ser Ser Lys Phe Arg Asp Glu Glu			
240	935	940	945	
241	gag tct ttt aca ctc cta tgc gac tgt gat gtc ctc gtg gcg cga tcc			5335
242	Glu Ser Phe Thr Leu Leu Ser Asp Cys Asp Val Leu Val Ala Arg Ser			
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Line ? Error/Warning

Original Text
